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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Sep 06 16:59:15 EDT 2007

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Reviewer Comments:

<110> TŠRECI, Šmzlem
SAHIN, Ugar
KREITER, Sebastian
Johannes Gutenberg-Universit, t Mainz, vertreten durch den
Pr, sidenten

Please remove all foreign accent marks: they are non-ASCII characters, and cannot be processed.

<210> 7

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Enzyme restriction site

Please try to clarify the above <223> response: can the source of the genetic material be mentioned? This type of response appears in Sequence 8.

<210> 11

<211> 1962

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid encoding a fusion protein

The above <223> response needs clarification: what are the sources of the fusion protein? This type of response appears in Sequence 13, too.

Application No: 10575640 Version No: 1.0

Input Set:

Output Set:

Started: 2007-08-27 08:37:14.100
Finished: 2007-08-27 08:37:17.698
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 598 ms
Total Warnings: 8
Total Errors: 0
No. of SeqIDs Defined: 66
Actual SeqID Count: 66

| Error code | Error Description |
|------------|---|
| W 213 | Artificial or Unknown found in <213> in SEQ ID (7) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (8) |
| W 402 | Undefined organism found in <213> in SEQ ID (9) |
| W 402 | Undefined organism found in <213> in SEQ ID (10) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (11) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (12) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (13) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (14) |

<210> 1
<211> 78
<212> DNA
<213> Homo sapiens

<400> 1
atgcgggtca cggcgccccg aaccctcatc ctgctgctct cgggagccct ggccctgacc 60
gagacacctggg ccggctcc 78

<210> 2
<211> 26
<212> PRT
<213> Homo sapiens

<400> 2

Met Arg Val Thr Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala
1 5 10 15

Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser
20 25

<210> 3
<211> 168
<212> DNA
<213> Homo sapiens

<400> 3
atcgtgggca ttgttgctgg cctggctgtc ctagcagttg tggtcatcg agctgtggtc 60
gctactgtga tgtgttaggag gaagagctca ggtggaaaag gagggagcta ctctcaggct 120
gcgtccagcg acagtgccca gggctctgat gtgtctctca cagcttga 168

<210> 4
<211> 55
<212> PRT
<213> Homo sapiens

<400> 4

Ile Val Gly Ile Val Ala Gly Leu Ala Val Leu Ala Val Val Val Ile
1 5 10 15

Gly Ala Val Val Ala Thr Val Met Cys Arg Arg Lys Ser Ser Gly Gly
20 25 30

Lys Gly Gly Ser Tyr Ser Gln Ala Ala Ser Ser Asp Ser Ala Gln Gly
35 40 45

Ser Asp Val Ser Leu Thr Ala

50

55

<210> 5

<211> 129

<212> DNA

<213> Homo sapiens

<400> 5

cagagcaaga tgctgagtgg agtcgggggc tttgtgctgg gcctgctctt ccttggggcc 60

ggcgtgttca tctacttcag gaatcagaaa ggacactctg gacttcagcc aagaggattc 120

ctgagctga 129

<210> 6

<211> 42

<212> PRT

<213> Homo sapiens

<400> 6

Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe Val Leu Gly Leu Leu

1 5 10 15

Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg Asn Gln Lys Gly His

20 25 30

Ser Gly Leu Gln Pro Arg Gly Phe Leu Ser

35

40

<210> 7

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Enzyme restriction site

<400> 7

ctgcaggcg actctagagg atcc 24

<210> 8

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Enzyme restriction site

<400> 8

Leu Gln Val Asp Ser Arg Gly Ser

1 5

<210> 9

<211> 1683

<212> DNA

<213> Cytomegalovirus

<400> 9

atggagtgcg cgggtcgccg ttgtccccaa atgatatccg tactgggtcc catttcgggg 60

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ctcctgcaga cgggtatcca cgtacgcgtg agccagccct cgctgatctt ggtatcgcag 180

tacacgcccc actcgacgcc atgccaccgc ggcgacaatc agctgcaggt gcagcacacg 240

tacttacgg gcagcgaggt ggagaacgtg tcggtaacg tgcacaaccc cacgggcccga 300

agcatctgcc ccagccagga gcccatgtcg atctatgtgt acgcgctgcc gctcaagatg 360

ctgaacatcc ccagcatcaa cgtgcaccac taccctgtcg cggccgagcg caaacaccga 420

cacctgcccc tagctgacgc tgtgattcac gcgtcgggca agcagatgtg gcaggcgctg 480

ctcacggctc cgggactggc ctggacgcgt cagcagaacc agtggaaaga gcccgcacgtc 540

tactacacgt cagcgttcgt gtttcccacc aaggacgtgg cactgcggca cgtggtgtgc 600

gcgcacgagc tggtttgctc catggagaac acgcgcgcaa ccaagatgca ggtgataggt 660

gaccagtacg tcaagggtgta cctggagtcc ttctgcgagg acgtgcgcctc cggcaagctc 720

tttatgcacg tcacgctggg ctctgacgtg gaagaggacc tgacgatgac ccgcaacccg 780

caacccttca tgcgc(cc)ca cgagcgcaac ggcttacgg tgggtgtcc caaaaatatg 840

ataatcaaac cgggcaagat ctcgcacatc atgctggatg tggctttac ctcacacgag 900

cattttgggc tgcgtgtcc caagagcatc cggggcctga gcatctcagg taacctgttg 960

atgaacgggc agcagatctt cctggaggta caagccatac gcgagaccgt ggaactgcgt 1020

cagtagcgtc cctggctgc gctttcttt ttcgatatcg acttgcgtct gcagcgccgg 1080

cctcagtaca gcgagcaccc cacccatc acccgatatac gcatccaggg caagctttag 1140

taccgacaca cctgggaccg gcacgacgag ggtgccccc agggcgacga cgacgtctgg 1200

accagcgat cggactccga cgaagaactc gtaaccaccc agcgcaagac gcccgcgtc 1260

accggcgccgc ggcgcattggc gggcgccctcc acttccgcgg gcccacaacg caaatcagca 1320

tcctcggcga cggcgtgcac gtcggggcggtt atgacacgcg gcccgcctaa ggcggagtcc 1380

accgtcgcbc ccgaagagga caccgacgag gattccgaca acgaaatcca caatccggcc 1440
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gctacggttc agggtcagaa tctgaagtac caggaattct tctggacgc caacgacatc 1560
taccgcatttc tcgccaattt ggaaggcgta tggcagcccg ctgcgcacc caaacgtcgc 1620
cgccaccggc aagacgcctt gcccgggcca tgcatcgccct cgacgccc aaagcacccga 1680
ggc 1683

<210> 10
<211> 561
<212> PRT
<213> Cytomegalovirus

<400> 10

Met Glu Ser Arg Gly Arg Arg Cys Pro Glu Met Ile Ser Val Leu Gly
1 5 10 15

Pro Ile Ser Gly His Val Leu Lys Ala Val Phe Ser Arg Gly Asp Thr
20 25 30

Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly Ile His Val
35 40 45

Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr Thr Pro Asp
50 55 60

Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val Gln His Thr
65 70 75 80

Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn Val His Asn
85 90 95

Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met Ser Ile Tyr
100 105 110

Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser Ile Asn Val
115 120 125

His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His Leu Pro Val
130 135 140

Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp Gln Ala Arg
145 150 155 160

Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn Gln Trp Lys
165 170 175

Glu Pro Asp Val Tyr Tyr Thr Ser Ala Phe Val Phe Pro Thr Lys Asp
180 185 190

Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val Cys Ser Met
195 200 205

Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp Gln Tyr Val
210 215 220

Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser Gly Lys Leu
225 230 235 240

Phe Met His Val Thr Leu Gly Ser Asp Val Glu Glu Asp Leu Thr Met
245 250 255

Thr Arg Asn Pro Gln Pro Phe Met Arg Pro His Glu Arg Asn Gly Phe
260 265 270

Thr Val Leu Cys Pro Lys Asn Met Ile Ile Lys Pro Gly Lys Ile Ser
275 280 285

His Ile Met Leu Asp Val Ala Phe Thr Ser His Glu His Phe Gly Leu
290 295 300

Leu Cys Pro Lys Ser Ile Pro Gly Leu Ser Ile Ser Gly Asn Leu Leu
305 310 315 320

Met Asn Gly Gln Gln Ile Phe Leu Glu Val Gln Ala Ile Arg Glu Thr
325 330 335

Val Glu Leu Arg Gln Tyr Asp Pro Val Ala Ala Leu Phe Phe Asp
340 345 350

Ile Asp Leu Leu Leu Gln Arg Gly Pro Gln Tyr Ser Glu His Pro Thr
355 360 365

Phe Thr Ser Gln Tyr Arg Ile Gln Gly Lys Leu Glu Tyr Arg His Thr

370

375

380

Trp Asp Arg His Asp Glu Gly Ala Ala Gln Gly Asp Asp Asp Val Trp
385 390 395 400

Thr Ser Gly Ser Asp Ser Asp Glu Glu Leu Val Thr Thr Glu Arg Lys
405 410 415

Thr Pro Arg Val Thr Gly Gly Ala Met Ala Gly Ala Ser Thr Ser
420 425 430

Ala Gly Arg Lys Arg Lys Ser Ala Ser Ser Ala Thr Ala Cys Thr Ser
435 440 445

Gly Val Met Thr Arg Gly Arg Leu Lys Ala Glu Ser Thr Val Ala Pro
450 455 460

Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His Asn Pro Ala
465 470 475 480

Val Phe Thr Trp Pro Pro Trp Gln Ala Gly Ile Leu Ala Arg Asn Leu
485 490 495

Val Pro Met Val Ala Thr Val Gln Gly Gln Asn Leu Lys Tyr Gln Glu
500 505 510

Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala Glu Leu Glu
515 520 525

Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg His Arg Gln
530 535 540

Asp Ala Leu Pro Gly Pro Cys Ile Ala Ser Thr Pro Lys Lys His Arg
545 550 555 560

Gly

<210> 11
<211> 1962
<212> DNA
<213> Artificial Sequence

<220>

<223> Nucleic acid encoding a fusion protein

<400> 11

| | | | | | | |
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| gagacctggg | ccggctccct | gcaggtcgac | tctagaggat | ccaccatgga | gtcgcgcggt | 120 |
| cgcgttgtc | ccgaaatgat | atccgtactg | ggtcccattt | cggggcacgt | gctgaaagcc | 180 |
| gtgttagtc | gcggcgatac | gccggtgctg | ccgcacgaga | cgcgactcct | gcagacgggt | 240 |
| atccacgtac | gcgtgagcca | gccctcgctg | atcttggtat | cgcagtacac | gcccgactcg | 300 |
| acgccatgcc | accggggcga | caatcagctg | caggtgcagc | acacgtactt | tacgggcagc | 360 |
| gaggtggaga | acgtgtcggt | caacgtgcac | aaccccacgg | gccgaagcat | ctgccccagc | 420 |
| caggagccca | tgtcgatcta | tgtgtacgca | ctgcccgtca | agatgctgaa | catccccagc | 480 |
| atcaacgtgc | accactaccc | gtcgccggcc | gagcgcaaac | accgacacct | gcccgttagct | 540 |
| gacgctgtga | ttcacgcgtc | gggcaagcag | atgtggcagg | cgcgtctcac | ggtctcgggta | 600 |
| ctggcctgga | cgcgtcagca | gaaccagtgg | aaagagcccg | acgtctacta | cacgtcagcg | 660 |
| ttcgtgtttc | ccaccaagga | cgtggactg | cggcacgtgg | tgtgcgcgca | cgagctggtt | 720 |
| tgctccatgg | agaacacgcg | cgcaaccaag | atgcaggtga | taggtgacca | gtacgtcaag | 780 |
| gtgtacctgg | agtccctctg | cgaggacgtg | ccctccggca | agctctttat | gcacgtcact | 840 |
| ctgggctctg | acgtggaaga | ggacctgacg | atgacccgca | acccgcaacc | cttcatgcgc | 900 |
| ccccacgagc | gcaacggctt | tacggtgttg | tgtcccaaaa | atatgataat | caaaccgggc | 960 |
| aagatctcgc | acatcatgct | ggatgtggct | tttacctcac | acgagcattt | tgggctgctg | 1020 |
| tgtcccaaga | gcatccgggg | cctgagcatc | tcaggttaacc | tgttgatgaa | cgggcagcag | 1080 |
| atcttccctgg | aggtacaagc | catacgcgag | accgtggaac | tgcgtcagta | cgatcccgtg | 1140 |
| gctgcgtct | tcttttcga | tatcgacttg | ctgctgcagc | gccccctca | gtacagcag | 1200 |
| cacccacct | tcaccagcca | gtatcgcatc | cagggcaagc | ttgagtaccg | acacacctgg | 1260 |
| gaccggcacg | acgagggtgc | cgtccaggggc | gacgacgacg | tctggaccag | cgatcggac | 1320 |
| tccgacgaag | aactcgtaac | caccgagcgc | aagacgcccc | gcgtcaccgg | cggcggcgcc | 1380 |
| atggcggggcg | cctccacttc | cgcggggccgc | aaacgcaaat | cagcatcctc | ggcgacggcg | 1440 |
| tgcacgtcg | gcgttatgac | acgcggccgc | cttaaggccg | agtccaccgt | cgcgccccaa | 1500 |
| gaggacaccc | acgaggattc | cgacaacgaa | atccacaatc | cggccgtgtt | cacctggccg | 1560 |
| ccctggcagg | ccggcatcct | ggcccccaac | ctggtgccca | tggtggtac | ggttcagggt | 1620 |

cagaatctga agtaccagga attcttctgg gacgccaacg acatctaccg catttcgcc 1680
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ggcattgttg ctggcctggc tgtccttagca gttgtggta tcggagctgt ggtcgctact 1860
gtgatgtgta ggaggaagag ctcaggtgga aaaggaggga gctactctca ggctgcgtcc 1920
agcgacagtg cccagggctc tgatgtgtct ctcacagctt ga 1962

<210> 12
<211> 653
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein

<400> 12

Met Arg Val Thr Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala
1 5 10 15

Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser Leu Gln Val Asp Ser Arg
20 25 30

Gly Ser Thr Met Glu Ser Arg Gly Arg Arg Cys Pro Glu Met Ile Ser
35 40 45

Val Leu Gly Pro Ile Ser Gly His Val Leu Lys Ala Val Phe Ser Arg
50 55 60

Gly Asp Thr Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly
65 70 75 80

Ile His Val Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr
85 90 95

Thr Pro Asp Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val
100 105 110

Gln His Thr Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn
115 120 125

Val His Asn Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met
130 135 140

Ser Ile Tyr Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser
145 150 155 160

Ile Asn Val His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His
165 170 175

Leu Pro Val Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp
180 185 190

Gln Ala Arg Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn
195 200 205

Gln Trp Lys Glu Pro Asp Val Tyr Tyr Thr Ser Ala Phe Val Phe Pro
210 215 220

Thr Lys Asp Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val
225 230 235 240

Cys Ser Met Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp
245 250 255

Gln Tyr Val Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser
260 265 270

Gly Lys Leu Phe Met His Val Thr Leu Gly Ser Asp Val Glu Glu Asp
275 280 285

Leu Thr Met Thr Arg Asn Pro Gln Pro Phe Met Arg Pro His Glu Arg
290 295 300

Asn Gly Phe Thr Val Leu Cys Pro Lys Asn Met Ile Ile Lys Pro Gly
305 310 315 320

Lys Ile Ser His Ile Met Leu Asp Val Ala Phe Thr Ser His Glu His
325 330 335

Phe Gly Leu Leu Cys Pro Lys Ser Ile Pro Gly Leu Ser Ile Ser Gly
340 345 350

Asn Leu Leu Met Asn Gly Gln Gln Ile Phe Leu Glu Val Gln Ala Ile
355 360 365

Arg Glu Thr Val Glu Leu Arg Gln Tyr Asp Pro Val Ala Ala Leu Phe
370 375 380

Phe Phe Asp Ile Asp Leu Leu Leu Gln Arg Gly Pro Gln Tyr Ser Glu
385 390 395 400

His Pro Thr Phe Thr Ser Gln Tyr Arg Ile Gln Gly Lys Leu Glu Tyr
405 410 415

Arg His Thr Trp Asp Arg His Asp Glu Gly Ala Ala Gln Gly Asp Asp
420 425 430

Asp Val Trp Thr Ser Gly Ser Asp Ser Asp Glu Glu Leu Val Thr Thr
435 440 445

Glu Arg Lys Thr Pro Arg Val Thr Gly Gly Ala Met Ala Gly Ala
450 455 460

Ser Thr Ser Ala Gly Arg Lys Arg Lys Ser Ala Ser Ser Ala Thr Ala
465 470 475 480

Cys Thr Ser Gly Val Met Thr Arg Gly Arg Leu Lys Ala Glu Ser Thr
485 490 495

Val Ala Pro Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His
500 505 510

Asn Pro Ala Val Phe Thr Trp Pro Pro Trp Gln Ala Gly Ile Leu Ala
515 520 525

Arg Asn Leu Val Pro Met Val Ala Thr Val Gln Gly Gln Asn Leu Lys
530 535 540

Tyr Gln Glu Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala
545 550 555 560

Glu Leu Glu Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg
565 570 575

His Arg Gln Asp Ala Leu Pro Gly Pro Cys Ile Ala Ser Thr Pro Lys
580 585 590

Lys His Arg Gly Gly Ser Ile Val Gly Ile Val